

FIGURE 54. Sequence similarity between SSeCKS (SEQ ID NO:4) and the Abl-binding domain in pRb. Identical a.a. residues (vertical lines) or similarly charged residues (colons) are shown for the SSeCKS and newt Rb (Genbank accession # Y09226) proteins.

On page 89, replace the last paragraph that continues on page 90, with the following paragraph:

Mapping of SSeCKS, as referred to herein as Gravin. Rodent SSeCKS and human Gravin/AKAP12 show 83% identity over the first ~1000 a.a., <20% similarity over the next ~500 a.a., and identity in two 15-a.a. stretches at the C-termini, one of which encodes a PKA anchoring site (Nauert et al., 1997, *Curr. Biol.* 7:52-62). Full-length SSeCKS cDNA recognizes Gravin mRNA under conditions of stringent hybridization (Gelman et al., 2000, *Histochem. J.* 32:13-26). Using a Gravin cDNA probe, human gravin was mapped by fluorescence in situ hybridization (FISH) to chromosome 6q24-25.2 (Fig. 43). These map coordinates are confirmed by microsatellite markers (Sanger Sequencing Centre, UK). Secondary hybridization signals were not detected which might reflect a second family member. FISH analysis using a full-length SSeCKS cDNA probe identified the same, singular region. Moreover, mouse SSeCKS maps to the Tsga12 locus at the centromeric end of chromosome 10p, which is syntenic with human chromosome 6q24-27⁴ strongly suggesting that SSeCKS and Gravin/AKAP12 are orthologues. Deletions in this region are associated with advanced, non-organ confined prostate cancer cases (Isaacs, et al., 1994, *Quant. Biol.* 59:653-659; Nupponen et al., 1998, *Cancer Genet. Cytogenet.* 101:53-57; Alers et al., 2000, *Lab. Investig.* 80:931-942; Crundwell et al., 1996, *Int. J. Cancer* 69:295-300; Bookstein, et al., 1997, *Br. J. Urol.* 79(Suppl 1):28-36; Srikantan et al., 1999, *Int. J. Cancer* 84:331-335; Visakorpi, T., 1999, *Ann. Chir. Gynaecol.* 88:11-16;